

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:49:42, Search time 18.214 seconds
(without alignments)
56.562 Million cell updates/sec

Title: US-09-856-070-16
Period start: 25
Sequence: 1 EREKE 5

Scoring table: RQSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DH seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_orquelelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriophage.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	25	100.0	57	Q19497	Q19497 caenorhabditis
2	25	100.0	61	Q9JUI4	Q9JUI4 neisseria m
3	25	100.0	62	10 064627	064627 arabidopsis
4	25	100.0	66	10 049518	049518 arabidopsis
5	25	100.0	80	048967	048967 mycoplasma
6	25	100.0	84	08X048	08X048 neurospora
7	25	100.0	85	13 091631	091631 xenopus lae
8	25	100.0	92	17 080172	080172 methanopyru
9	25	100.0	94	080172	080172 methanopyru
10	25	100.0	104	10 091398	091398 oryza sativ
11	25	100.0	106	2 05K113	05K113 clostridium
12	25	100.0	111	3 090104	090104 schistosom
13	25	100.0	117	1 090104	090104 schistosom
14	25	100.0	117	5 0814X8	0814X8 plasmodium
15	25	100.0	121	4 075438	075438 homo sapien
16	25	100.0	121	4 075438	075438 homo sapien

17	25	100.0	121	4 080008	080008 homo sapien
18	25	100.0	121	5 0815A1	0815A1 plasmodium
19	25	100.0	121	11 090841	090841 mus musculus
20	25	100.0	123	5 095221	095221 plasmodium
21	25	100.0	123	5 081548	081548 plasmodium
22	25	100.0	123	16 0923V1	0923V1 helicobacte
23	25	100.0	124	5 095075	095075 plasmodium
24	25	100.0	126	5 096453	096453 plasmodium
25	25	100.0	128	13 091607	091607 xenopus lae
26	25	100.0	140	14 091608	091608 xenopus lae
27	25	100.0	130	13 090887	090887 gallus gall
28	25	100.0	135	10 080872	080872 narcissus p
29	25	100.0	136	10 080872	080872 narcissus p
30	25	100.0	137	5 090894	090894 plasmodium
31	25	100.0	137	10 091809	091809 arabidopsis
32	25	100.0	141	11 090841	090841 mus musculus
33	25	100.0	145	17 080172	080172 methanopyru
34	25	100.0	152	4 090128	090128 homo sapien
35	25	100.0	152	4 090128	090128 homo sapien
36	25	100.0	158	4 090128	090128 homo sapien
37	25	100.0	158	11 090128	090128 mus musculus
38	25	100.0	159	2 090128	090128 mus musculus
39	25	100.0	159	4 090128	090128 mus musculus
40	25	100.0	160	13 091506	091506 xenopus lae
41	25	100.0	161	4 090128	090128 homo sapien
42	25	100.0	161	10 080128	080128 oryza sativ
43	25	100.0	168	16 092045	092045 listeria in
44	25	100.0	175	4 090128	090128 mus musculus
45	25	100.0	175	4 015608	015608 homo sapien

ALIGNMENTS

RESULT 1

Q19497 PRELIMINARY; PRT: 57 AA.
AC Q19497
DT 01-NOV-1996 (FIREHIREL. 01, Created)
DT 01-NOV-1996 (FIREHIREL. 01, Last sequence update)
DT 01-DEC-2001 (FIREHIREL. 19, Last annotation update)
DE Hypothetical 7.9 kDa protein.
GN FL6H11.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phabditida; Phabditidae.
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99099613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
PL Science 262:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Wu X.;
FT "The sequence of C. elegans cosmid FL6H11.";
EL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
FT "Direct submission.";
EL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
OP F001: 055476; AAA98006.1;
KW Hypothetical protein.
SQ SEQUENCE 57 AA: 7899 MW: 315876A323688010 CRC64:

Query Match: 100.0%, Score 25, E-Val: 1.6e-02;
Best local similarity: 100.0%, E-Val: 1.6e-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

IIIIII

DB 48 EREKE 52

RESULT 2

Q4J014 PRELIMINARY: PRT: 61 AA.
 AC Q4J014:
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein NMA1295.
 GN NMA1295.
 OS Neisseria meningitidis (serogroup A).
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CX NCBI_TaxID=69599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN 22491, J. SEROTYPE 4A.
 RX MEDLINE=20242556; PubMed=10761919.
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.P., Morelli G., Busham D., Brown D., Chillingworth T., Davies R.M., Davis F., Devlin K., Feilwell T., Hamlin N., Holroyd S., Jacobs K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skilton J., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491".
 RI Nature 404:502-506(2000).
 RL Nature 404:502-506(2000).
 DR EMBL: A162755; CAH84547.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 61 AA: 7525 MW: A029B40BFA5EFA49 CRC64:

Query Match 100.0%; Score 25; DB 16; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

IIIIII

DB 32 EREKE 36

RESULT 3

Q64627 PRELIMINARY: PRT: 62 AA.
 AC Q64627:
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DE 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DE 01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
 DE At2g18970 protein.
 GN At2g18970.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 CC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN CV, Columbia;
 RX MEDLINE=20084487; PubMed 10617197;
 RA Liu X., Kaul S., Rounsley S.D., Shea E.P., Benito M.-L., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V., Buell C.R., Ketchum K.A., Lee J.-J., Rounsley C.M., Koo H., Mehlert K.S., Cronin L.A., Shen M., VanAken S.E., Maynard D., Tallon L.J., Gill J.E., Adams M.D., Carrara A., Crayshaw T.H., Goodman H.M., Somerville C.R., Chapple C.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana".
 RI Nature 402:761-768(1999).
 RL Nature 402:761-768(1999).

QY 1 EREKE 5
 IIIIII
 DB 53 EREKE 57

Query Match 100.0%; Score 25; DB 10; Length 62;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

IIIIII

DB 53 EREKE 57

RESULT 4

Q49518 PRELIMINARY: PRT: 66 AA.
 AC Q49518:
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DE 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Hypothetical 8.1 kDa protein.
 GN F2432.160 OR A14618500.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 CC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Bancroft I., Moses H.W., Mayer K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Moses H.W., Lemcke K., Mayer K.P.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1021710; CAA16730.1; -.
 DR EMBL: A1161548; CAH78852.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA: 8086 MW: F850CDB9E8E06224 CRC64:

Query Match 100.0%; Score 25; DB 10; Length 66;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

IIIIII

DB 15 EREKE 23

RESULT 5

Q48967 PRELIMINARY: PRT: 80 AA.
 AC Q48967:
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Similar to serine protease RE (Fragment).
 OS Mycoplasma capricolum.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 CC Entomoplasmatales; Entomoplasmataceae.
 CX NCBI_TaxID=2095;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN-ATCC 27343(KID);
FX MEDLINE-96059641; PubMed 7476192;
RA Bork P., Ouzounis C., Casari C., Schneider R., Sander C., Dolan M.,
RI Gilbert W., Gillevet P.M.;
RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
RT its physiology.";
RL Mol. Microbiol. 16:955-967(1995).
DR EMBL: Z33027; CAA83706.1; -.
KW Protease.
FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA: 9695 MW: 101675.5335080 CRG64,
Query Match 100.0%; Score 25; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 46 EREKE 50
|||||
RESULT 6
Q8X0A8 PRELIMINARY; PPT: 84 AA.
ID Q8X0A8 PRELIMINARY; PPT: 84 AA.
AC Q8X0A8 PRELIMINARY; PPT: 84 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DE Hypothetical 9.0 kDa protein.
GN B14D6.200
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
OC Sordariates; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schullie U., Aign V., Hehseisel J., Brandt P., Fartmann B., Holland P.,
RA Nykatura G., Mewes H.W., Mandhaupt G.;
RI Submitted (MAY-2000) to the EMBL/GenBank/DBI databases
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBI databases.
DR EMBL: AL356173; CAB91729.2;
KW Hypothetical protein.
SQ SEQUENCE 84 AA: 8972 MW: 100180.08080 CRG64,
Query Match 100.0%; Score 25; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.2e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 39 EREKE 43
|||||
RESULT 7
Q91631 PRELIMINARY; PPT: 85 AA.
ID Q91631 PRELIMINARY; PPT: 85 AA.
AC Q91631 PRELIMINARY; PPT: 85 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DE XE2.1 protein (fragment).
GN XE2.1
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

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RA Neuman T., Zuber M.X.;
RI Submitted (MAY-1995) to the EMBL/GenBank/DBI databases.
DR EMBL: U35055; AAA78933.1; -.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH_1.
DR SMART: SM00353; HLH; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 85 85
SQ SEQUENCE 85 AA: 10083 MW: 1039875.672068660 CRG64,
Query Match 100.0%; Score 25; DB 13; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.3e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 3 EREKE 7
|||||
RESULT 8
Q8TUZ2 PRELIMINARY; PPT: 92 AA.
ID Q8TUZ2 PRELIMINARY; PPT: 92 AA.
AC Q8TUZ2 PRELIMINARY; PPT: 92 AA.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DE Chitinase mutase.
GN PHA OK M1509.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RA STEIN-AN19 / DSM 6324 / DSM 9639;
EX MEDLINE-21927647; PubMed-11930014;
RA Shcherbina A.V., Mecheraya K.V., Makarova K.S., Polushin N.M.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Nalae P.A., Begonin I.B., Tarasov P.I., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Kozlov E.V., Kozlovkin S.A.;
RI "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RI and morphology of archaeal methanogens.";
DE PubMed Nalae P.A., Steinhilber S.A., 99:444-464;(2002).
DE EMBL: AL010156; AAM92822.1; -.
KW Complete proteome.
SQ SEQUENCE 92 AA: 10623 MW: 1090400.49888 CRG64,
Query Match 100.0%; Score 25; DB 17; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 47 EREKE 51
|||||
RESULT 9
Q9BGY7 PRELIMINARY; PPT: 94 AA.
ID Q9BGY7 PRELIMINARY; PPT: 94 AA.
AC Q9BGY7 PRELIMINARY; PPT: 94 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DE 01 DEC 2001 (TrEMBLrel. 19, last annotation update)
DE Hypothetical 10.7 kDa protein.
OS Macaca fascicularis (Orangutan macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FRONTAL LOBE LEFT;

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KA Osada N., Hida M., Kusuda J., Tanuma K., Iseki K., Hirai M., Ierao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.,
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBP databases
 DR EMBL: AB055270; HAH21894.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 94 AA; 10698 MW; 14771AAC3543EAD0 CRC64;

Query Match 100.0%; Score 25; DB 6; Length 94;
 Best local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 52 EREKE 56
 |||||

RESULT 10

QYLG38 PRELIMINARY; PRT: 104 AA.
 AC QYLG38;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE P0462H08.20 protein.
 GN P0462H08.20.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 CX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.,
 RT "Oryza sativa nipponbare(CA) genomic DNA, chromosome 1, PAC
 clone: P0462H08."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBP databases.
 DR EMBL: AP002525; BAB07997.1; -
 SQ SEQUENCE 104 AA; 11434 MW; A3DDE6295G4CE76D CRC64;

Query Match 100.0%; Score 25; DB 10; Length 104;
 Best local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 99 EREKE 103
 |||||

RESULT 11

QYKIT3 PRELIMINARY; PRT: 106 AA.
 AC QYKIT3;
 DI 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE SpoIIIG (Fragment).
 OS Clostridium sporosches.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 CX NCBI_TaxID=1509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE:20340964; PubMed:10878124;
 RA Arcuri E.F., Wiedmann M., Boor K.J.;
 RT "Phylogeny and functional conservation of Sigma E in endospore-forming
 bacteria."
 RL Microbiology 146:1593-1604(2000).
 DR EMBL: AF225466; AAF35486.1; -
 DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; sigma70; 1.

FT NON_TER 1 1
 FT NON_TER 106 106
 SQ SEQUENCE 106 AA; 12446 MW; F5144CE29A7C153C CRC64;
 Query Match 100.0%; Score 25; DB 2; Length 106;
 Best local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 82 EREKE 86
 |||||

RESULT 12

QYUTJ4 PRELIMINARY; PRT: 111 AA.
 AC QYUTJ4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Hypothetical coiled-coil protein.
 GN SPAC1556.05C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 CX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Saunders D., Harris D., McQuail R.C., Rajandream M.A., Barrell B.G.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBP databases.
 DR EMBL: AL132984; CAB61216.1; -
 SQ SEQUENCE 111 AA; 13513 MW; C9C87C83E241568D CRC64;

Query Match 100.0%; Score 25; DB 3; Length 111;
 Best local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 50 EREKE 54
 |||||

RESULT 13

QYHH91 PRELIMINARY; PRT: 117 AA.
 AC QYHH91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 14.3 kDa protein.
 OS Sulfolobus islandicus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 CX NCBI_TaxID=43080;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HN7H2;
 RA MEDLINE:20510146; PubMed:11054382;
 RA Peng X., Holz L., Zillig W., Garrett K.A., She Q.;
 RT "Evolution of the family of PRN plasmids and their integrase-mediated
 insertion into the chromosome of the crenarchaeon Sulfolobus
 J. Mol. Biol. 303:449-454(2000).
 RL EMBL: AJ294536; CAC15942.1; -
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 117 AA; 14348 MW; D4CC45252C1F78A1 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 117;
 Best local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: January 16, 2003, 16:55:37
 Job Time : 20.2143 secs

QY 1 EREKE 5
 |||||
 DB 112 EREKE 116

RESULT 14

QRT4X8

ID Q814X8 PRELIMINARY: PRT: 117 AA.
 AC Q814X8;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Erythrocyte membrane protein 1 (Fragment).
 GN VAR.
 GS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID:5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PH4;
 RX MEDLINE:21839615; PubMed:11849711;
 RT Fowler E.V., Peters J.M., Gattton M.H., Chen N., Cheng Q.;
 RA "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
 RL genes among Asia-Pacific isolates."
 BT Mol Biochem Parasitol. 120:117-126(2002).
 DR EMBL: AF054934; AAL11298.1; -.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13871 MW; BC1E0F0548B7BEB8 CRC64;

Query Match

100.0%; Score 25; DB 5; Length 117.

Best Local Similarity 100.0%; Prod. No. 3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 18 EREKE 22

RESULT 15

075408

ID 075408 PRELIMINARY: PRT: 120 AA.
 AC 075408;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE Huntingtin interacting protein HYPK (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Faber P.W., Barnes G.T., Srinidhi J., Chen J., Gusella J.F.,
 RA MacDonald M.R.;
 RT "Huntingtin interacts with a family of WW domain proteins."
 RL Hum. Mol. Genet. 0:0-0(1998).
 DR EMBL: AF049613; AAC26849.1; -.
 FT NON_TER 1
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13520 MW; 0CF2C487B3FF230B CRC64;

Query Match

100.0%; Score 25; DB 4; Length 120.

Best Local Similarity 100.0%; Prod. No. 3.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 71 EREKE 75

